

OIPE

## RAW SEQUENCE LISTING

DATE: 12/19/2001

PATENT APPLICATION: US/09/817,014

TIME: 15:57:22

Input Set : A:\SEQLISTVANM213001AUS.TXT

Output Set: N:\CRF3\12192001\I817014.raw

ENTERED

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4 <110> APPLICANT: Remacle, Jose
5      Hamels, Sandrine
6      Zammattéo, Nathalie
7      Lockman, Laurence
8      Dufour, Sophie
9      Alexandre, Isabelle
10     De Longueville, Francoise
13 <120> TITLE OF INVENTION: IDENTIFICATION OF BIOLOGICAL
14     (MICRO)ORGANISMS BY DETECTION OF THEIR HOMOLOGOUS NUCLEOTIDE
15     SEQUENCES ON ARRAYS
17 <130> FILE REFERENCE: VANM213.001AUS
19 <140> CURRENT APPLICATION NUMBER: US 09/817,014
20 <141> CURRENT FILING DATE: 2001-03-23
22 <150> PRIOR APPLICATION NUMBER: EP 00870055.1
23 <151> PRIOR FILING DATE: 2000-03-24
25 <150> PRIOR APPLICATION NUMBER: EP 00870204.5
26 <151> PRIOR FILING DATE: 2000-09-15
28 <160> NUMBER OF SEQ ID NOS: 192
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 23
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: primer for amplification of S. aureus
40 <400> SEQUENCE: 1
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43 <210> SEQ ID NO: 2
44 <211> LENGTH: 25
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: primer for amplification of S. aureus
51 <400> SEQUENCE: 2
52 tttattttaa atatacagct cttcg                25
54 <210> SEQ ID NO: 3
55 <211> LENGTH: 23
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: primer for amplification of S. epidermidis
62 <400> SEQUENCE: 3
63 tcgcggtcca gtaatagatt ata                23
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 22
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence

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70 <220> FEATURE:
71 <223> OTHER INFORMATION: primer for amplification of S. epidermidis
73 <400> SEQUENCE: 4
74 tgcatttcca gttatttctc cc 22
76 <210> SEQ ID NO: 5
77 <211> LENGTH: 24
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: primer for amplification of S. haemolyticus
84 <400> SEQUENCE: 5
85 attgatcatg gtattgatag atac 24
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 25
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: primer for amplification of S. haemolyticus
95 <400> SEQUENCE: 6
96 tttaatcttt ttgagtgtct tatac 25
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 25
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: primer for amplification of S. saprophyticus
106 <400> SEQUENCE: 7
107 taaaatgaaa caactcgggtt ataag 25
109 <210> SEQ ID NO: 8
110 <211> LENGTH: 24
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: primer for amplification of S. saprophyticus
117 <400> SEQUENCE: 8
118 aaactatcca taccattaag tacg 24
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 24
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: primer for amplification of S. hominis
128 <400> SEQUENCE: 9
129 cgaccagata acaaaaaagc acaa 24
131 <210> SEQ ID NO: 10
132 <211> LENGTH: 22
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:

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137 <223> OTHER INFORMATION: primer for amplification of S. hominis
139 <400> SEQUENCE: 10
140 gtaattcggtt accatgttct aa 22
142 <210> SEQ ID NO: 11
143 <211> LENGTH: 27
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: capture nucleotide ATaur02
150 <400> SEQUENCE: 11
151 attttaaata tcacgtctctt cgttttag 27
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154 <211> LENGTH: 27
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: capture nucleotide ATepi02
161 <400> SEQUENCE: 12
162 attaagcaca tttctttcat tattttag 27
164 <210> SEQ ID NO: 13
165 <211> LENGTH: 27
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: capture nucleotide ATHae02
172 <400> SEQUENCE: 13
173 attttaaagtt tcacgttcat tttgtaa 27
175 <210> SEQ ID NO: 14
176 <211> LENGTH: 27
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: capture nucleotide ATHom02
183 <400> SEQUENCE: 14
184 atttaatgtc tgacgttctg catgaag 27
186 <210> SEQ ID NO: 15
187 <211> LENGTH: 27
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: capture nucleotide ATsap02
194 <400> SEQUENCE: 15
195 acttaatact tcgcgttcag cctttaa 27
197 <210> SEQ ID NO: 16
198 <211> LENGTH: 24
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: consensus primer APstap03

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205 <400> SEQUENCE: 16
206 cccaactcgct tatatagaat ttga                24
208 <210> SEQ ID NO: 17
209 <211> LENGTH: 23
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: consensus primer APstap04
216 <400> SEQUENCE: 17
217 ccactagcgt acatcaattt tga                23
219 <210> SEQ ID NO: 18
220 <211> LENGTH: 25
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: consensus primer APstap05
227 <400> SEQUENCE: 18
228 ggtttaataa agtcaccaac atatt                25
230 <210> SEQ ID NO: 19
231 <211> LENGTH: 47
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: capture nucleotide (with spacer sequence) ATepi03
238 <221> NAME/KEY: misc_feature
239 <222> LOCATION: (1)...(20)
240 <223> OTHER INFORMATION: spacer sequence
242 <400> SEQUENCE: 19
243 gaattcaaag ttgctgagaa attaagcaca tttctttcat tatttag                47
245 <210> SEQ ID NO: 20
246 <211> LENGTH: 67
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: capture nucleotide (with spacer sequence) ATepi04
253 <221> NAME/KEY: misc_feature
254 <222> LOCATION: (1)...(40)
255 <223> OTHER INFORMATION: spacer sequence
257 <400> SEQUENCE: 20
258 gaattcaaag ttgctgagaa tagttcaatg gaaggaagcg attaagcaca tttctttcat 60
259 tatttag                                     67
261 <210> SEQ ID NO: 21
262 <211> LENGTH: 87
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: capture nucleotide (with spacer sequence) ATepi05
269 <221> NAME/KEY: misc_feature
270 <222> LOCATION: (1)...(60)

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271 <223> OTHER INFORMATION: spacer sequence
273 <400> SEQUENCE: 21
274 gaattcaaaag ttgctgagaa tagttcaatg gaaggaagcg tcttctttaa atctaaagaa 60
275 attaagcaca tttctttcat tattttag 87
277 <210> SEQ ID NO: 22
278 <211> LENGTH: 67
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: capture nucleotide (with spacer sequence) Ataur27
285 <221> NAME/KEY: misc_feature
286 <222> LOCATION: (1)...(40)
287 <223> OTHER INFORMATION: spacer sequence
289 <400> SEQUENCE: 22
290 gaattcaaaag ttgctgagaa tagttcaatg gaaggaagcg attttaaata tcacgtctctt 60
291 cgttttag 67
293 <210> SEQ ID NO: 23
294 <211> LENGTH: 67
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: capture nucleotide (with spacer sequence) Atepi27
301 <221> NAME/KEY: misc_feature
302 <222> LOCATION: (1)...(40)
303 <223> OTHER INFORMATION: spacer sequence
305 <400> SEQUENCE: 23
306 gaattcaaaag ttgctgagaa tagttcaatg gaaggaagcg attaagcaca tttctttcat 60
307 tattttag 67
309 <210> SEQ ID NO: 24
310 <211> LENGTH: 67
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: capture nucleotide (with spacer sequence) Athae27
317 <221> NAME/KEY: misc_feature
318 <222> LOCATION: (1)...(40)
319 <223> OTHER INFORMATION: spacer sequence
321 <400> SEQUENCE: 24
322 gaattcaaaag ttgctgagaa tagttcaatg gaaggaagcg atttaaagtt tcacgttcat 60
323 ttgttaa 67
325 <210> SEQ ID NO: 25
326 <211> LENGTH: 67
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: capture nucleotide (with spacer sequence) Athom27
333 <221> NAME/KEY: misc_feature
334 <222> LOCATION: (1)...(40)
335 <223> OTHER INFORMATION: spacer sequence

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VERIFICATION SUMMARY

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L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28

L:1526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128